AUTHOR INDEX

VOLUME 154

Ahmed, Zia U., 239
Aiba, Shuichi, 831
Aizawa, Shin-ichi, 84
Akporiaye, Emmanuel T., 520
AliKhan, M. Y., 1168
Allen, Mary Mennes, 1480
Andreesen, Jan R., 192
Asoh, Sadamitsu, 10
Atkinson, Katharine D., 1276
Atlung, Tove, 443
Aud, Janet C., 1168

Baca, Oswald G., 520
Backman, Keith C., 516
Bagdasarian, M., 676
Balows, Albert, 324
Barak, Rina, 1431
Barbour, Alan G., 1436
Barnsley, E. A., 113
Barr, Kathleen, 1245
Bayer, Edward A., 893
Bayly, Ronald C., 1363
Beachey, Edwin H., 139
Beatty, J. Thomas, 1440
Beckwith, Jon, 253, 356, 366
Bellion, Edward, 1168
Bennett, Michael F., 1389
Berg, Howard C., 312
Berger-Bächi, Brigitte, 479, 533
Bird, Robert E., 1174
Block, Steven M., 312
Boileau, Guy, 1323
Bolbot, John A., 1168
Boman, Hans G., 170
Bonato, Maria C. Manhães, 1467
Boye, Erik, 656
Bradley, David E., 505
Brady, G., 429
Bragg, Philip D., 708, 719
Brañes, Lucia V., 1462
Bremer, H., 787
Brown, Teresa M., 269
Buckley, J. T., 413
Burdett, Ian D. J., 1389
Burgdorfer, Willy, 1436
Burris, Robert H., 351
Bussey, Howard, 161
Buu, Antoinette, 130
Buxton, Roger S., 1309
Buzby, Jeffrey S., 1446
Byeon, Woo-Hyeon, 1252

Callahan, James P., 1455
Callister, Heather, 537
Calvo, Joseph M., 1054
Campbell, Judith L., 809
Canepari, Pietro, 916
Cantu, Mona, 632
Card, George L., 294
Carey, V. C., 1291
Carman, George M., 304
Chakrabarty, A. M., 1356
Champe, Sewell P., 955
Chandler, R. E., 1222
Chang, Ying-Ying, 756
Charon, Nyles W., 846
Chassy, Bruce M., 819, 1195, 1204
Chaudhry, G. Rasul, 387
Chen, Hui-Zhu, 650
Chen, Yu-Mei, 516
Cheng, Soo-Chen, 1005
Chesney, Robert H., 513
Chet, Ilan, 1431
Childs, Warren D., III, 1110
Chung, Chin Ha, 231
Clark, David, 554
Clark, W. Gregg, 580
Clarke, Patricia H., 508
Coetzee, Jack N., 505
Cohen, Helga, 460
Cohen, Stanley N., 580, 1440
Comai, Luca, 1162
Cookson, Brad T., 1126
Cox, B. S., 612
Coyette, Jacques, 916
Craven, Rebecca C., 780
Crawford, Irving P., 1455
Crofton, Sylvia, 58
Cronan, John E., Jr., 221, 554, 756
Crooks, Jane H., 1009
Crouch, Robert J., 1021
Cryz, Stanley J., Jr., 245

da Costa Maia, José C., 1467
Dahlberg, James E., 529
Danbara, H., 429
Daneo-Moore, Lolita, 573
Date, Takayasu, 76
Davis, Bernard D., 1215, 1381
Davis, Rowland H., 1046
Deal, Carolyn D., 1015
Dean, Gary E., 84
DeFelice, Maurilio, 1054
de Graaf, Frits K., 41
Del Casale, Thomas, 513
de Louvencourt, Laurence, 737
de Mendoza, Diego, 221
Dennis, Patrick P., 58
de Smet, Marie J., 870
De Wit, René J. W., 859
Dickson, Robert C., 1245
Dobrogosz, Walter J., 992
Drews, G., 471
Drury, Lucy S., 1309
Dubnau, D., 1077
Dürre, Peter, 192
Durrens, Pascal, 702
Dworkin, Martin, 437, 452, 772

Eccleshall, T. R., 1301
Eggink, Gerrit, 870
Eide, David, 437
Eisenbach, Michael, 604
Elad, Yigal, 1431
Ely, Bert, 1137
Evans, Dolores G., 980
Evans, Doyle J., Jr., 980
Evans, R. Paul, Jr., 1347

Federoff, H. J., 1301
Ferber, Donna M., 1137
Ferenci, Thomas, 984
Ferrari, Franco A., 1513
Ferri, Mariella, 118
Finan, Turlough M., 1403
Finch, Lloyd R., 17
Finn, Donald J., 294
Fischl, Anthony S., 304
Fiske, Michael J., 623
Flouret, Bernard, 1284
Fonseca, Rocío, 146
Fontana, Roberta, 916
Fouser, Lynette, 1174
Fraenkel, Dan G., 1002
Franklin, F. C. H., 676
Fraser, Murray J., 460
Freese, Ernst, 261
Frey, J., 429
Friedberg, Errol C., 1459
Friedrich, Cornelius G., 803
Fuchs, James A., 1040
Fujii, Mikio, 831
Fujita, Tamie, 864
Fujita, Yasutaro, 864
Fukuhara, Hiroshi, 737
Furukawa, Hidehiko, 938
Furukawa, Kensuke, 1356
Futcher, A. B., 612

Gardner, Jeffrey F., 287
Gardner, John S., 499, 502
Garwin, Jeffrey L., 221
Gasson, Michael J., 1
Gennis, Robert B., 1269
Georgopoulos, Costa, 1505
Ghazi, Alexandre, 92
Ghosh, A., 946
Ghosh, B. K., 946
Gibson, Carolyn W., 573
Giffin, Kelleen, 554
Goebel, W., 1145
Goebel, Werner, 200
Goldberg, Alfred L., 231
Gómez-Eichelmann, M. Carmen, 1493
Green, George N., 1269
Guarente, Leonard, 356
Gutnick, David L., 893
Guzmán-Verduzco, Luz María, 146

Hacker, J., 1145
Hackett, Neil R., 708, 719

Hackstadt, Ted, 591, 598
Hammer-Jespersen, Karin, 72
Hanke, Paul D., 1040
Hanne, Larry F., 383
Hansen, Flemming G., 443
Hansen, Grethe E., 443
Hansen, Tonny D., 72
Hase, Tatsuo, 879, 976
Hashimoto, Tadayo, 965
Hawley, Marguerite A., 1480
Hayes, Stanley F., 1436
Hearst, John E., 748
Hector, R. F., 488
Hedges, Robert W., 505
Helmstetter, Charles E., 1371
Hermann, Theron E., 955
Hernández, Georgina, 524
Heslot, Henri, 737
Hess, Gerard F., 1455
Hess, Wilford M., 499, 502
Higgins, Michael L., 573
Hille, Jacques, 693
Hitchcock, Penny J., 269
Hoch, James A., 1088, 1513
Holbein, Bruce E., 728
Holmes, Randall K., 245
Horinouchi, Sueharu, 1252
Horiuchi, Seikoh, 1215, 1381
Houlberg, U., 1485
Hove-Jensen, B., 1485
Hove-Jensen, Bjarne, 177
Howard, S. P., 413
Howe, John G., 1323
Howe, Timothy R., 383
Hughes, E. John, 1363
Hughes, Kelly T., 1126
Hugouvieux-Cotte-Pattat, Nicole, 663
Hunt, J. C., 793
Hus, W. H., 1033
Hutchins, Kendrick, 161

Iglewski, Barbara H., 383
Ikeuchi, Toshihiko, 988
Im, Dong-Soo, 803
Imae, Yasuo, 104
Imanaka, Tadayuki, 831
Ingram, L. O., 1291
Inouye, Hiroshi, 366
Ishida-Schick, Tamako, 1276
Ishino, Yumiko, 1476
Izawa, Seikichi, 185

Jensen, Roy A., 623
Jochimsen, B., 1485
Johnson, Reid C., 1137
Jones, Robert B., 998
Jordan, D. Carlyle, 1403
Josephsen, Jytte, 72
Juliani, Maria H., 1467
Jürgens, U. J., 471

Kanaya, Shigenori, 1021
Kaplan, Samuel, 1015
Kawasaki, Glenn, 1002
Kay, William W., 1462
Keithly, James H., 838
Kent, Mary E., 1168
Kerszman, Gustaw, 443
Kingma, Jaap, 870
Kinney, Sandra G., 1397
Kitada, Makio, 330
Klasen, Ina, 693
Knapp, S., 1145
Kneifel, Helmut, 1315
Konijn, Theo M., 859
Kooistra, Jan, 686
Kosuge, Tsune, 1162
Krawiec, Steven, 1027
Krilowicz, Beverly L., 1276
Kronstad, J. W., 419
Krulwich, Terry A., 330
Kudoh, Jun, 988
Kumamoto, Carol A., 253
Kumar, R., 946
Kumar, Sharad, 65
Kumazawa, Shuzo, 185
Kupersztoch-Portnoy, Yankel M., 146
Kurahashi, Kiyoshi, 988
Kuroiwa, Tsuneyoshi, 938
Kurtz, Myra Berman, 955

Ladika, Dubravka, 1126
LaDuca, Richard J., 1371
Lago, Carmine T., 1054
Lambert, John M., 1323
Lang, Dennis, 1513
Lange, Charles F., 965
Laverack, Peter D., 508
Lee, Jong Ho, 992
Lee, Kin-Sang, 984
LeGall, Jean, 278
Lehrbach, P. R., 676
Leish, Brian A., 1276
Levy, Stuart B., 1009
Lewis, Richard J., 330
Little, R., 787
Liu, Ming-Cheh, 278
Lopez, Juan M., 261
Loughney, Kate, 529
Lowry, R. K., 1222
Luke, Richard K. J., 1263
Lund, Elsebet, 529
Lurz, R., 676
Lutkenhaus, Joseph F., 1339
Lynn, Steven P., 287

MacGregor, C. H., 387
Mackie, George A., 152
Macnab, Robert M., 84
Macrina, Francis L., 1347
Magasanik, Boris, 516
Magee, B. B., 1033
Magee, P. T., 1033
Maloy, Stanley R., 561
Marmiroli, Nelson, 118
Marmur, J., 1301
Marrs, Barry L., 580, 748
Marty-Mazars, Daniele, 1215, 1381
Masson, Luke, 728
Matsuhashi, Michio, 10
Matsuzawa, Hiroshi, 10
Matthysse, Ann G., 906
Mattingly, Stephen J., 211
Mayer, Leonard W., 1498
McEwen, Joan, 375
McFall, Elizabeth, 1508
McGinness, T., 537
McMeekin, T. A., 1222
Mengin-Lecreulx, Dominique, 1284
Menichi, Bernadette, 130
Michaelis, Susan, 356, 366
Miller, Charles G., 763
Miller, Richard D., 1104
Mitchell, Alana, 17
Mitsui, Akira, 185
Mizushima, Shoji, 669, 938
Model, Peter, 1064
Modrich, Paul, 1005
Montie, Thomas C., 780
Mooi, Frits R., 41
Mora, Jaime, 524
Morse, Stephen A., 1104
Moser, David R., 809
Moses, Robb E., 1459
Mukhopadhyay, Pradip, 1098
Murray, Barbara E., 980

Nadler, Kenneth D., 838
Neale, Geoffrey A. M., 17
Neidhardt, Frederick C., 336, 344, 1505
Neilands, J. B., 324
Nelson, David R., 547
Nettleton, David O., 1088
Neuhaus, Francis C., 1110
Newhall, Wilbert J., V, 998
Nguyen, Ahn, 1513
Nicholas, D. J. D., 65
Nunn, William D., 554
Nygaard, P., 1485

Ofek, Itzhak, 139
Ogasawara, Naotake, 50
Ogrydziak, David M., 23
Ohta, Takahisa, 10
Oliver, Don, 366
Olivera, Baldomero M., 1126
Ono, Bun-Ichiro, 1476
Oosawa, Kenji, 104
Ordal, George W., 1088
Orndorff, Paul, 772
Ozawa, Yuji, 669

Palacios, Rafael, 524
Palchaudhuri, Sunil, 1098
Pang, Patty P., 1502
Pappagianis, D., 488
Parsons, Gaylene D., 152
Pattee, P. A., 395, 406

Payne, William J., 278
Peck, Harry D., Jr., 278
Peñaranda, Maria E., 980
Pera, Kate A., 1236
Peterson, David E., 846
Pfister, Robert M., 924
Phibbs, P. V., Jr., 793
Pine, Leo, 324
Pines, Ophry, 893
Pollack, Jordan H., 965
Porter, Ronald D., 1446
Privalle, Laura Stein, 351
Puglisi, Pier P., 118

Quesneau, Yves, 663

Ramirez, Robert M., 1276
Rashtchian, Ayoub, 1009
Rasmussen, Knud V., 443
Ratkowsky, D. A., 1222
Ravid, Shoshana, 604
Reddy, C. A., 1033
Reeves, Michael W., 324
Reissig, Jose L., 1397
Ristow, Janet L., 1046
Rittenberg, S. C., 32
Robbins, Kenneth E., 1498
Robert-Baudouy, Janine, 663
Rosen, Barry P., 854
Roth, John R., 561, 1126
Ruby, E. G., 32
Rueckert, B., 676
Runkel, Laura, 1508
Rupp, W. Dean, 1459
Russel, Marjorie, 1064
Russell, Lesley M., 245
Ryals, J., 787

Said, Suraia, 1472
Salyers, Abigail A., 287
Sambucetti, Lidia, 375
Sancar, Aziz, 1459
Sánchez-Pescador, Ray, 524
Sargent, Michael G., 1389
Sargentini, Neil J., 743
Satta, Giuseppe, 916
Schecter, J. B., 1329
Scherer, Paul, 1315
Schilperoort, Rob, 693
Schnepf, H. E., 419
Schoonejans, Eric, 1489
Schultz, Roger A., 1459
Segall, Jeffrey E., 312
Seiki, Motoharu, 50
Sharma, Rakesh C., 743
Sharma, Surendra, 1459
Shechter, Emanuel, 92
Shinoda, Sumio, 1476
Sicard, Nicole, 995
Sidén, Inga, 170
Silver, Pamela, 569
Silverman, Philip M., 375
Simon, John R., 1356
Skarstad, Kirsten, 656
Smith, Kendric C., 743
Smith, Martin W., 336, 344
Sollitti, Paul, 513
Somerson, Norman L., 924
Squires, Charles H., 1054
Staehelin, L. Andrew, 1414
Stahl, Mark L., 395, 406
Stahl, Susan J., 930
Starich, Todd, 772
Steen, Harald B., 656
Stellwag, Edmund, 772
Stevens, S. E., Jr., 1446
Stewart, Kenneth R., 930
Stokes, A. N., 1222
Strauch, Kathryn L., 763
Sueoka, Noboru, 1184
Syrowik, Ursula, 1098

Tai, Phang C., 1215, 1381
Takagi, Masahiro, 831
Takagi, Tsutomu, 1153
Tanaka, Teruo, 1184
Taron, Douglas J., 1110
Taylor, Dean P., 580
Terenzi, Héctor F., 1472
Tesh, Martha J., 1104
Tetaz, Timothy J., 1263
Therisod, Hélène, 92
Thomas, Edwin L., 1236
Thompson, John, 819, 1195, 1204
Thompson, Lucile Wawzonek, 1027
Tilly, Kit, 1505
Timmis, K. N., 429, 676
Torres, Haydée K., 1493
Toussaint, Ariane, 1227, 1489
Traut, Robert R., 1323
Tripathi, R. K., 502
Tsujibo, Hiroshi, 854

Ueno-Nishio, Shizue, 516
Ulrich, Amy Klages, 221
Uratani, Brenda, 261

VanBogelen, Ruth A., 1505
van Boxel, Theo, 686
Van Der Velden, Rob J., 859
Van Gijsegem, Frédérique, 1227
van Heijenoort, Jean, 1284
van Kan, Jan, 693
Varga, Amy R., 1414
Vary, Patricia S., 1455
Venema, Gerard, 686
Vining, Leo C., 239
Vogel, Monika, 200

Wagner, Wilma, 200
Wake, R. G., 537
Walker, Graham C., 1117, 1502
Wall, Frances, 924
Walsh, R. Brian, 1002
Warner, Huber R., 1451
Watson, Terence G., 1013
Weckesser, J., 471
Weinrauch, Y., 1077
Weisblum, Bernard, 1252
Wesolowski, Micheline, 737
Westfall, Helen N., 846
Whitaker, Robert J., 623
Whiteley, H. R., 419
Whitman, W. B., 640
Whitnack, Ellen, 139
Wickner, William, 569
Wijffjes, André, 41
Williams, Fred D., 930
Williams, Jim C., 598
Winans, Stephen C., 1117
Witholt, Bernard, 870
Wolfe, R. S., 640
Wood, Janet M., 1403
Wynberg, Hans, 870

Yamada, Tetsuji, 23
Yasuda, Seiichi, 1153
Yeung, Maria K., 211
Yoch, Duane C., 632
Yoshikawa, Hiroshi, 50
Youvan, Douglas C., 748

Zhang, Zhao-Ming, 632
Zissler, James, 772
Zubay, Geoffrey, 650
Zusman, David R., 547

SUBJECT INDEX
VOLUME 154

Acid proteases, extracellular
  S. lipolytica, 23
Acinetobacter calcoaceticus
  cell surface emulsan, 893
Adenine nucleotide levels
  Anabaena sp. strain 7120, 351
Aerobiosis
  E. coli, 344
  protein induction, 344
Aeromonas hydrophila
  protein export mutants, 413
Agmenellum quadruplicatum
  plasmid transformation, 1446
Agrobacterium tumefaciens
  cellulose fibrils, 906
  site-directed mutagenesis in *E. coli* of R772::Ti, 693
D-Alanyl-lipoteichoic acid synthesis
  L. casei, 1110
  role of diglyceride kinase in phosphatidylglycerol synthesis, 1110
Alcaligenes eutrophus
  meta-cleavage pathway, 1363
  ribulosebisphosphate carboxylase formation
    fluoride, 803
    formate, 803
    hydrogen, 803
Aldohexuronate transport
  E. carotovora, 663
Alkaline phosphatase secretion-negative mutant
  B. licheniformis, 946
Alkaline phosphatase signal sequence
  E. coli mutants, 366
Amino acid utilization
  L. pneumophila, 1104
6-Aminonicotinamide resistance
  S. typhimurium, 1126
Anabaena sp. strain 7120
  adenine nucleotide levels, 351
  nitrogen fixation, 351
Anaerobiosis
  E. coli, 336
  protein induction, 336
ansA
  L-asparaginase, 513
  E. coli, 513
Aphanocapsa
  cyanophycin granule polypeptide
    protein degradation, 1480
    synthesis, 1480
Apurinic-apyrimidinic endonuclease activity
  E. coli mutant, 1459
araC, mutations in
  E. coli, 1329
argF
  expression
    E. coli, 508
    P. aeruginosa, 508
    P. putida, 508
ars
  yeast cloning vector containing *ars* from *C. utilis*, 1033
L-Asparaginase
  ansA, 513
  E. coli mutant, 513
Aspergillus nidulans
  laccase, 955
ATP
  M. bryantii, 640
  methylreductase system, activation of, 640

Bacillus firmus
  respiratory chain, 330
Bacillus licheniformis
  alkaline phosphatase secretion-negative mutant, 949
Bacillus megaterium
  trp-his region, 1455
Bacillus stearothermophilus
  phospholipid metabolism, 294
  thermostabe neutral protease gene
    cloned in plasmid pTB90 and expressed in *B. stearothermophilus* and *subtilis*, 831
Bacillus subtilis
  B. stearothermophilus thermostable neutral protease gene, 831
  cell division, 537
  chemotaxis
    genetics, 1088
  complexed membrane
    proteins, 1215
  decoyinine, 261
  DNA-membrane interactions, 1389
  Δ*igf*, 864
  integrable plasmid, 1513
  peptidoglycan synthesis and turnover, 261
  plasmid marker rescue transformation, 1077
  plasmid pBD221, 1077
  plasmid pUB110 binding to membrane fraction, 1184
  proteins of ribosome-bearing and free-membrane domains, 1381
  rRNA gene set, deletion set, 529
  rRNA operons near chromosomal origin, 50
  spo0A and *spo0C* cloned onto phage ρ11, 988
  ts1 division initiation product, 537
Bacillus thuringiensis
  crystal protein genes, 419
Bacteriophage
  I. dammini, 1436
  Lyme disease, 1436
Bacteriophage chi
  E. coli chemotaxis, 604
Bacteriophage f1
  E. coli fip, 1064
Bacteriophage IKe
  $IncI_2$ plasmids specify sensitivity to, 505
Bacteriophage MX8

lysogeny in *M. xanthus*, 772
Bacteriophage ρ11
spo0A and *spo0C* cloned onto, 988
Bacteriophage T4
DNA injection into *E. coli*, 938
Bacteriophage T5
E. coli, 130
overproduction of receptor protein, 130
Bacteroides
cloned DNA used for identification, 287
Base excision repair
Thermus sp. strain X-1, 1451
Bdellovibrio bacteriovorous
differentiation, 32
Biphenyl catabolism
P. paucimobilis, 1356
Blastocladiella emersonii zoospores
cyclic nucleotide-independent protein kinases, 1467
phosphorylation of a single 40S ribosomal subunit protein, 1467

Calcium as a branching signal
N. crassa, 1397
Calcium efflux
E. coli, 854
energetics, 854
canI
nonsense mutations, 1476
S. cerevisiae, 1476
2'-Carboxybenzalpyruvate formation
phenanthrene metabolism
phthalate pathway, 113
Candida utilis
ars, yeast cloning vector containing, 1033
Catabolite repression
aerobic and anaerobic shock, 992
E. coli mutants, 992
Catalase activity
C. burnetii, 520
Caulobacter crescentus
fla mutants, 1137
cdd
E. coli, 72
C_4-dicarboxylic acid transport mutants
R. leguminosarum, 1403
symbiotic properties, 1403
Cecropin D
E. coli mutants, 170
Cell cycle parameters
E. coli, slowly growing, 656
Cell division
B. subtilis, 537
coupled with DNA replication, 1339
E. coli, 1339
sulB is an allele of *ftsZ*, 1339
Cell surface emulsan
A. calcoaceticus, 893
Cellulose fibrils
A. tumefaciens infection, 906
Cell wall
peptidoglycan synthesis
Streptococcus protoplasts, 211
Cell wall receptor
(1→6)-β-D-glucan, 161
yeast killer toxin, 161
Chemotaxis
adaptation kinetics, 312
B. subtilis, 1088
E. coli, 104, 312
E. coli
phage chi, 604
genetics, 1088
methylation, 780
M. xanthus, 437
P. aeruginosa, 780
repellent
ethylene glycol, 104
glycerol, 104
Chitin, nonfibrillar
T. mentagrophytes arthrospores, 965
Chitin synthesis
C. immitis, 488
inhibition by polyoxin D, 488
Chlamydiae
outer membrane protein
disulfide-linked oligomers, 998
chl mutants
E. coli cytochromes, 719
Chloramphenicol production
S. venezuelae, 239
Chromatium sp. strain Miami PBS1071
H_2 oxidation, 185
proton efflux, 185
Chromosome replication
E. coli dnaA mutants, 1371
Cloning
Bacteroides species identification with cloned DNA, 287
E. carotovora genes involved in hexuronate catabolism, 1227
genes that complement yeast hexokinase and glucokinase mutants, 1002
pbpA, 10
pnp, 58
rodA, 10
spo0A and *spo0C* of *B. subtilis* onto phage ρ11, 988
thermostable neutral protease gene from *B. stearothermophilus*, 830
Clostridia
glycine metabolism, 192
purine metabolism, 192
Coccidioides immitis
chitin synthesis, 488
polyoxin D, 488
Complexed membrane
B. subtilis, 1215
proteins, 1215
Copper resistance
E. coli, 1263
Copy number
plasmid pMB1, 809
RNA I gene dosage, 809
Corynebacterium diphtheriae
iron transport, 245
toxigenesis, regulation of, 245
Coxiella burnetii
catalase activity, 520
cytoplasmic pH, 591
glutamate transport, 591
proton motive force, 591
superoxide anion production, 520
superoxide dismutase activity, 520
cpxA cpxB mutants

E. coli, 375
outer membrane protein synthesis, 375
Crystal protein genes
B. thuringiensis, 419
Culture growth rate
model, 1222
Cyanophycin granule polypeptide
Aphanocapsa, 1480
protein degradation, 1480
synthesis, 1480
Cyclic nucleotide-independent protein kinases
ribosomes of *B. emersonii* zoospores, 1467
cyd
E. coli, 1269
Cytidine deaminase
cdd, 72
E. coli, 72
Cytochrome *d* terminal oxidase
E. coli mutant, 1269
Cytochromes
E. coli
chl mutants, 719
grown aerobically and anaerobically with nitrate, 708
P. perfectomarinus, 278
Cytoplasmic pH
C. burnetii, 591

Decoyinine
B. subtilis, 261
peptidoglycan synthesis and turnover, 261
2-Deoxy-D-glucose
S. lactis
glycolysis, 819
phosphotransferase activities, 819
Dictyostelium minutum
folic acid C_9-N_{10}-cleaving enzyme, 859
Differentiation
B. bacteriovorous, 32
Disulfide-linked oligomers
chlamydial outer membrane protein, 998
DNA
cloned fragments used for *Bacteroides* spp. identification, 287
DnaG protein
plasmid ColE1 replication, 1174
DNA injection
phage T4 infection of *E. coli*, 938
DNA-membrane interactions
B. subtilis, 1389
DNA polymerase deficiency
E. coli, 1098
trimethoprim, 1098
DNA replication
coupled with cell division, 1339
E. coli, 1339
H. influenzae transformation, 686
sulB is an allele of *ftsZ*, 1339
DNA replication control
E. coli rpoC mutant, 443
DNA sequences
E. coli, 1508
D-serine deaminase control region and N-terminal portion of the structural gene, 1508
dye (*sfrA*)
dye sensitivity, 1309
E. coli, 1309
sex factor F expression, 1309

Elongation factor G
E. coli growth cycle, 1323
Emulsan-like polymers
A. calcoaceticus, 893
Endo-exonuclease
N. crassa, 460
Endonuclease
plasmid pKM101 coded, 1117
Enterotoxin, heat-stable
E. coli, 146
thermoactivation, 146
Erwinia carotovora
aldohexuronate transport, 663
hexuronate catabolism genes
cloning, 1227
Erwinia carotovora subsp. *chrysanthemi*
plasmid pULB113 (RP4::mini-Mu) used to construct a linkage map, 1489
Erythromycin
S. cerevisiae
protein synthesis, 118
sporulation, 118
Escherichia coli
aerobiosis, 344
alkaline phosphatase signal sequence mutants, 366
anaerobiosis, 336
ansA, 513
apurinic-apyrimidinic endonuclease activity, 1459
araC, mutations in, 1329
argF expression, 508
L-asparaginase, 513
calcium efflux, 854
cdd, 72
cecropin D sensitivity, 170
cell cycle parameters, 656
cell division, 1339
chemotaxis, 104, 312, 604
chl mutants, 719
chromosome replication, 1371
copper resistance, 1263
cpxA cpxB mutants, 375
cyclic AMP suppressor mutants
aerobic and anaerobic shock, 992
catabolite repression, 992
cyd, 1269
cytidine deaminase, 72
cytochrome *d* terminal oxidase, 1269
cytochromes, 708, 719
cytoplasmic serine protease, 231
dnaA mutants, 1371
DNA polymerase deficiency, 1098
DNA replication, 1339
DNA replication control, 443
dye sensitivity, 1309
dye (*sfrA*), 1309
elongation factor G, 1323
enterotoxin, heat-stable, 146
fabF, 221
fadR, 554
fatty acid synthesis, unsaturated, 554
fip, 1064
ftsZ, 1339
glnL product, 516

groES gene product, 1505
guanosine tetraphosphate, 787
heat-inducible protein C15.4, 1505
heat-stable enterotoxin, 146
hemolysin determinant, 1145
hemolysin transport, 200
$hlyB_a$, $hlyB_b$, 220
K88ab fimbria, synthesis of, 41
lac carrier, 92
lactose uptake, 92
lamB mutants, 984
leader peptidase, 76
lep, 569
mapping, new approach, 569
membrane lipid composition, 221
minichromosome replication, 1371
mmrA1, 743
ompC, 669
ompF, 669
mutagenesis of R772::Tn, 693
nitrate reductase subunit A, 387
nitrogen assimilation, 516
nrd mRNA synthesis, 1040
N-terminal region of the structural gene
DNA sequence, 1508
outer membrane porin protein synthesis, 669
outer membrane protein synthesis, 375
pbpA, 10
peptidoglycan synthesis, 1284
phage chi, 604
phage f1 assembly, 1064
phage T4 DNA injection, 938
phage T5 receptor, 130
phoA-lacZ gene fusions, 356
phosphoribosylpyrophosphate synthetase, 177
plasmid R100 stability, 1493
plasmid R1-19 stability, 1493
pnp, 58
polynucleotide phosphorylase gene, 58
poxB mutation, 756
protease So, 231
protein C15.4, 1505
protein induction, 336, 344
protein localization, 253
protein, replication, 1153
protein synthesis, 375
prs, 177
purG, 1485
purI, 1485
receptor protein, 130
replication proteins
overproduction, 1153
ribonucleoside diphosphate reductase mRNA synthesis, 1040
ribosomal protein S1, 1323
ribosomal protein S20, 152
ribosome synthesis, 787
rodA, 10
rod shape
pbpA, 10
rodA, 10
rpoB mutation, 787
rpoC mutant, 443
rpsT, 152
secB, 253
D-serine deaminase control region
DNA sequence, 1508
sex factor F expression, 1309
site-directed mutagenesis of R772::Tn, 693
ST:LT:CFA/II plasmids, 980
sulB is an allele of *ftsZ*, 1339
trimethoprim, 1098
UDP *N*-acetylglucosamine-enolpyruvate pool levels, 1284
UDP *N*-acetylglucosamine pool levels, 1284
unsaturated fatty acid synthesis, 554
UV irradiation
minimal medium recovery, 743
mmrA1, 743
postreplication repair, 743
Ethanol
Z. mobilis lipid, 1291
Ethylene glycol
chemotaxis repellent, 104
E. coli, 104
Extracellular acid proteases
S. lipolytica, 23
Extracellular slime
P. mirabilis swarming, 930

fabF
E. coli, 221
fadR
E. coli, 554
unsaturated fatty acid synthesis, 554
Fatty acid synthesis, unsaturated
E. coli, 554
fadR, 554
fip
E. coli, 1064
filamentous phage f1 assembly, 1064
flaAII
S. typhimurium, 84
Flagellin
C. crescentus, 1137
fla mutants
C. crescentus, 1137
Fluorescence mutants
R. capsulata, 748
Fluoride
ribulosebisphosphate carboxylase formation in *A. eutrophus*, 803
Folic acid C_9-N_{10}-cleaving enzyme
D. minutum, 859
Formate
ribulosebisphosphate carboxylase formation in *A. eutrophus*, 803
Fruiting body formation
M. xanthus, 547
protein S translocation, 547

Galactose-PEP-dependent PTS system
L. casei, 1204
glnL product
E. coli, 516
nitrogen assimilation, 516
(1→6)-β-D-Glucan
yeast killer toxin receptor, 161
Gluconeogenesis
M. rouxii, 1472
Glucose
Z. mobilis lipid, 1291

Glucose catabolism
P. aeruginosa, 793
Glucose-dependent growth control
modE, 702
Podospora mutant, 702
Glutamate dehydrogenase NADP synthesis
N. crassa, 524
nitrogen source, 524
Glutamate transport
C. burnetii, 598
pH, 598
Glutamine synthetase-chromatophore association
R. rubrum, 632
Glycerol
chemotaxis repellent, 104
E. coli, 104
Glycine metabolism
clostridia, 192
Glycolysis
S. lactis, 819
groES gene product
E. coli, 1505
heat-inducible protein C15.4, 1505
Growth
modE, 702
Podospora, 702
Growth pattern
R. tsutsugamushi in irradiated L cells, 879
Growth rate
model, 1222
Guanosine tetraphosphate
E. coli, 787
ribosome synthesis, 787
rpoB mutation, 787

Haemophilus influenzae
Rec-1 protein, 686
transformation
DNA replication, 686
Heat-inducible protein C15.4
groES gene product of *E. coli*, 1505
Heat-stable enterotoxin
E. coli, 146
thermoactivation, 146
Hemolysin determinant
E. coli O6 strain, 1145
Hemolysin transport
E. coli outer membrane, 220
hlyB$_a$, *hlyB*$_b$, 220
D-*glycero*-D-*manno*-Heptose
S. typhimurium LPS core mutants, 1462
Hexadecane droplets
S. pyogenes adherence, 139
Hexuronate catabolism
E. carotovora genes, 1227
hlyB$_a$, *hlyB*$_b$
E. coli, 220
H_2 oxidation
Chromatium sp. strain Miami PBS1071, 185
proton efflux, 185
Hydrogen
ribulosebisphosphate carboxylase formation in *A. eutrophus*, 803

Δ*igf*
B. subtilis, 864

ilvHI
S. typhimurium, 1054
Inclusions
octane-grown *P. oleovorans*, 870
Iron deficiency
Legionella spp.
siderophore activity, 324
Iron transport
C. diphtheriae, 245
IS*51*
causes mutations in a plant pathogenic *Pseudomonas* sp., 1162
Isoleucine biosynthesis
pathway in *Leptospira*, 846
Ixodes dammini
Lyme disease, 1436
phage, 1436

K88ab fimbria, synthesis of
E. coli, 41
Killer plasmid DNA
K. lactis, 737
transformation, 737
Kluyveromyces lactis
killer plasmid DNA
transformation, 737
lactose transport, 1245

lac carrier
E. coli, 92
lactose uptake, 92
Laccase
A. nidulans
cleistothecial primordia, 955
Hulle cells, 955
β-Lactams
mode of action, 916
S. faecium, 916
Lactobacillus casei
D-alanyl-lipoteichoic acid synthesis, 1110
galactose-PEP-dependent PTS, 1204
lactose-PEP-dependent PTS, 1195
β-D-phosphogalactoside galactohydrolase activity, 1195
Lactose-PEP-dependent PTS
L. casei, 1195
Lactose transport
K. lactis, 1245
Lactose uptake
E. coli, 92
lac carrier, 92
lamB mutants
E. coli, 984
Leader peptidase
E. coli, 76
Leader peptidase gene (*lep*)
E. coli, 569
mapping, new approach for, 569
Lectins
mycoparasitism, 1431
Legionella pneumophila
intermediary metabolism, 1104
Legionella spp.
siderophore activity, 324
lep
E. coli, 569

mapping, new approach for, 569
Leptospira
isoleucine biosynthesis pathways, 846
lexA gene product
uvrD of *S. typhimurium*, 1502
Lipid
ethanol, 1291
glucose, 1291
Z. mobilis, 1291
Lipopolysaccharide core mutants
S. typhimurium, 1462
Lipopolysaccharide heterogeneity
Salmonella mutants with different LPS chemotypes, 269
Lyme disease
I. dammini
phage, 1436
Lysogeny
phage MX8 in *M. xanthus*, 772

Macrolide, lincosamide, streptogramin B resistance
S. sanguis, 1252
Maltase synthesis
S. carlsbergensis, 1301
Mapping cloned genes, new approach, 569
Mapping, computer-assisted, 395
Membrane, complexed
B. subtilis, 1215
proteins, 1215
Membrane differentiation
R. palustris, 1414
Membrane-DNA interactions
B. subtilis, 1389
Membrane lipid composition
fabF, 221
E. coli mutants, 221
Membrane, outer
E. coli cpxA cpxB mutants, 375
protein synthesis
meta-cleavage pathway
A. eutrophus, 1363
Methanobacterium bryantii
methylreductase system, activation by ATP, 640
Methanogens
polyamine distribution, 1315
Methanol uptake
Pseudomonas sp. strain AM1, 1168
Methicillin resistance
inactivation by Tn*551*, 479
S. aureus, 479
transposon Tn*551* transduction efficiency, 533
Methylamine uptake
Pseudomonas sp. strain AM1, 1168
Methylation
P. aeruginosa chemotaxis, 780
Methylreductase system
ATP activation, 640
M. bryantii, 640
Minichromosome replication
E. coli dnaA mutants, 1371
mmrA1
E. coli, 743
UV irradiation
minimal medium recovery, 743
postreplication repair, 743
modE
glucose-dependent growth control, 702
Podospora, 702
Motility
C. crescentus mutants, 1137
flaAII, 84
S. typhimurium, 84
Mucor rouxii
gluconeogenesis, 1472
Mycoparasitism
lectins, 1431
Mycoplasma mycoides subsp. *mycoides*
pyrimidine deoxyribonucleotide synthesis, 17
Mycoplasma pneumoniae
tip structure, 924
Myxococcus xanthus
chemotaxis, 437
fruiting body formation, 547
lysogeny by phage MX8, 772
protein S translocation, 547
tactic behavior, 452

Neisseria gonorrhoeae
plasmid pMR0360
evolutionary analysis, 1498
Neisseria meningitidis
sialic acid capsular polysaccharide synthesis, 728
Neurospora crassa
calcium as a branching signal, 1397
endo-exonuclease, 460
glutamate dehydrogenase NADP synthesis, 524
mitochondrial membrane, 1046
nitrogen, 524
ornithine cycle, 1046
Nitrate reductase subunit A
E. coli, 387
Nitrobacter agilis
proton gradient, 65
Nitrogen
glutamate dehydrogenase NADP synthesis, 524
N. crassa, 524
Nitrogen assimilation
E. coli, 516
glnL product, 516
Nitrogen fixation
Anabaena sp. strain 7120, 351
Nitrosomas europaea
proton gradient, 65
Nonfibrillar chitin
T. mentagrophytes arthrospores, 965
nrd mRNA synthesis
E. coli, 1040
N-terminal region of the structural gene
DNA sequence, 1508
E. coli, 1508

n-Octane
P. oleovorans grown on
inclusions, 870
ompC
E. coli, 669
ompF
E. coli, 669
Ornithine cycle
mitochondrial membrane, 1046
N. crassa, 1046

Outer membrane
protein synthesis
E. coli cpxA cpxB mutants, 375
Outer membrane porin protein synthesis
E. coli, 669
ompC, 669
ompF, 669
Outer membrane protein
chlamydiae, 998
disulfide-linked oligomers, 998
Oxygen metabolism
S. mutans, 1236

pbpA
E. coli, 10
Penicillin-binding proteins
S. faecium growth, 916
Peptidase T mutants
S. typhimurium, 763
Peptidoglycan
B. subtilis, 261
decoyinine, 261
Synechocystis sp. strain PCC 6714, 471
Peptidoglycan synthesis
E. coli, 1284
Streptococcus protoplasts, 211
UDP *N*-acetylglucosamine-enolpyruvate pool levels, 1284
UDP *N*-acetylglucosamine pool levels, 1284
pH
C. burnetii
cytoplasmic, 591
glutamate transport, 598
proton motive force, 598
Phenanthrene metabolism
2′-carboxybenzalpyruvate formation, 113
phthalate pathway, 113
L-Phenylalanine
overflow pathway to, 623
P. aeruginosa, 623
phoA-lacZ gene fusions
E. coli, 356
Phosphatidylinositol synthase, microsome-associated
S. cerevisiae, 304
β-D-Phosphogalactoside galactohydrolase activity
L. casei, 1195
Phospholipid metabolism
B. stearothermophilus, 294
Phospholipid synthesis
S. cerevisiae mutants, 1276
Phosphoribosylpyrophosphate synthetase
E. coli, 177
prs, 177
Photosynthesis
R. capsulata chromosome, 580
Photosynthesis genes
R. capsulata, 1440
hybridization with DNA from photosynthetic bacteria, 1440
Phthalate pathway
2′-carboxybenzalpyruvate formation, 113
phenanthrene metabolism, 113
Plasma membrane expansion
S. cerevisiae mutants, 1276
Plasmid ColE1
early replicative intermediates, 1174
expression in vitro after chromosome fragmentation, 650
Plasmid curing
streptococcal protoplasts, 1
Plasmid DNA replication
pMB1, 809
regulation, 809
Plasmid marker rescue transformation
B. subtilis, 1077
Plasmid 2μm
S. cerevisiae, 612
Plasmid pBD221
B. subtilis, 1077
marker rescue transformation, 1077
Plasmid pIP501, 1347
Plasmid pKM101-coded endonuclease, 1117
Plasmid pMB1 copy number mutant
RNA I gene dosage
copy number, 809
incompatability, 809
Plasmid pMR0360
evolutionary analysis, 1498
N. gonorrhoeae, 1498
Plasmid pUB110
binding to *B. subtilis* membrane fraction, 1184
Plasmid pULB113 (RP4::mini-Mu)
E. carotovora subsp. *chrysanthemi* linkage map, 1489
Plasmid R100
stability in *E. coli* and *S. typhimurium*, 1493
Plasmid R1-19
stability in *E. coli* and *S. typhimurium* strains, 1493
Plasmid R6-5
replication control mutations, 429
Plasmid R772::Ti
A. tumefaciens, 693
E. coli, 693
Plasmids $IncI_2$
phage IKe, sensitivity to, 505
Plasmid transformation
A. quadruplicatum, 1446
pnp
cloning, 58
E. coli, 58
Podospora
glucose-dependent growth control, 702
modE, 702
Polyamine distribution
methanogens, 1315
Polynucleotide phosphorylase
cloning of gene, 58
E. coli, 58
Polyoxin D
chitin synthesis, 488
C. immitis, 488
Polysaccharide antigen synthesis
Streptococcus protoplasts, 211
poxB mutation
E. coli, 756
Proline utilization
put::Mu *d*(Ap, *lac*), 561
S. typhimurium, 561
Protease So
E. coli cytoplasmic serine protease, 231
Protease (thermostable neutral) gene from *Bacillus stearothermophilus*
cloning in plasmid pTB90, 831

expression in *B. stearothermophilus* and *B. subtilis*, 831
Protein
B. subtilis complexed membrane, 1215
Protein C15.4
E. coli groES gene product, 1505
Protein export
A. hydrophila mutants, 413
Protein induction
E. coli
aerobiosis, 344
anaerobiosis, 336
Protein localization
E. coli, 253
secB, 253
Protein, replication
E. coli, 1153
overproduction, 1153
Proteins
B. subtilis
ribosome-bearing and free-membrane domains, 1381
M. xanthus fruiting body formation, 547
translocation, 547
Protein S1
E. coli growth cycle, 1323
Protein synthesis
E. coli cpxA cpxB mutants, 375
erythromycin, 118
S. cerevisiae, 118
sporulation, 118
Proteus mirabilis
extracellular slime during swarming, 930
Proton efflux
Chromatium sp. strain Miami PBS1071, 185
H_2 oxidation, 185
Proton gradients
N. agilis, 65
N. europaea, 65
Proton motive force
C. burnetii, 591
Protoplast fusion
computer-assisted chromosome mapping, 395
S. aureus, 395
Protoplast-induced curing
streptococci, 1
Protoporphyrin formation
R. japonicum, 838
prs
E. coli, 177
phosphoribosylpyrophosphate synthetase, 177
Pseudomonas aeruginosa
argF expression
E. coli, 508
P. aeruginosa, 508
P. putida, 508
chemotaxis
methylation, 780
glucose catabolism, 793
L-phenylalanine, pathway to, 623
toxA1, 383
Pseudomonas oleovorans
inclusions in octane-grown cells, 870
Pseudomonas paucimobilis
biphenyl catabolism, 1356
salicylate catabolism, 1356
xylene/toluene catabolism, 1356
Pseudomonas perfectomarinus
cytochromes, 278
Pseudomonas putida
argF expression, 508
Pseudomonas sp.
IS*51*, 1162
Pseudomonas sp. strain AM1
methanol uptake, 1168
methylamine uptake, 1168
purG
E. coli, 1485
enzymatic reaction encoded by, 1485
purI
E. coli, 1485
enzymatic reaction encoded by, 1485
Purine metabolism
clostridia, 192
put::Mu *d*(Ap, *lac*) operon fusions
proline utilization, regulation of, 561
S. typhimurium, 561
Pyrimidine deoxyribonucleotide synthesis
M. mycoides subsp. *mycoides*, 17
Pyruvate oxidase
poxB mutation in *E. coli*, 756

Receptor
(1→6)-β-D-glucan, 161
yeast killer toxin, 161
Receptor protein
E. coli, 130
phage T5, 130
Repair
transformability correlated with deficiency in error-prone repair, 995
Replication
chromosome and minichrome
E. coli dnaA mutants, 1371
Replication control mutations
plasmid R6-5, 429
Replication origin
B. subtilis chromosome, 50
rRNA operons, 50
Respiratory chain
B. firmus, 330
Rhizobium japonicum
protoporphyrin formation, 838
Rhizobium leguminosarum
dicarboxylic acid transport mutants
symbiotic properties, 1403
Rhizoctonia solani
lectins, 1431
Rhodopseudomonas capsulata
fluorescence mutants, 748
hybridization of cloned photosynthesis genes with DNA from other photosynthetic bacteria, 1440
photosynthesis region of chromosome, 580
Rhodopseudomonas palustris
membrane differentiation, 1414
Rhodospirillum rubrum
glutamine synthetase-chromatophore association, 632
Ribonucleoside diphosphate reductase mRNA synthesis
E. coli, 1040
Ribosomal protein S1
E. coli growth cycle, 1323

Ribosomal protein S20
E. coli, 152
expression of gene, 152
Ribulosebisphosphate carboxylase formation
A. eutrophus, 803
fluoride, 803
formate, 803
hydrogen, 803
Rickettsia tsutsugamushi
growth pattern in irradiated L cells, 879
progeny assembly in irradiated L cells, 976
RNA I gene dosage
plasmid pMB1
copy number, 809
incompatability, 809
rodA
E. coli, 10
rpoB mutation
E. coli, 787
ribosome synthesis, 787
rpoC mutant
DNA replication control, 443
E. coli, 443
rpsT expression
E. coli, 152
rRNA gene set, deletion of
B. subtilis, 529
rRNA operons
B. subtilis chromosome, 50

Saccharomyces cerevisiae
can1 nonsense mutations, 1476
cloning of genes that complement hexokinase and glucokinase mutants, 1002
erythromycin, 118
killer toxin
(1→6)-β-D-glucan, 161
receptor, 161
phosphatidylinositol synthase, microsome-associated, 304
phospholipid synthesis, 1276
plasma membrane, 1276
plasmid 2μm maintenance, 612
protein synthesis, 118
secretion-defective mutants
phospholipid synthesis, 1276
plasma membrane expansion, 1276
sporulation, 118
Saccharomyces carlsbergensis
maltase synthesis, 1301
Saccharomycopsis lipolytica
extracellular acid proteases, 23
Salicylate catabolism
P. paucimobilis, 1356
Salmonella
lipopolysaccharide heterogeneity, 269
Salmonella typhimurium
6-aminonicotinamide resistance, 1126
flaAII, 84
ilv HI, 1054
LPS core mutants containing D-*glycero*-D-*manno*-heptose, 1462
motility, 84
peptidase T mutants, 763
plasmid R100 stability, 1493
plasmid R1-19 stability, 1493
proline utilization, regulation of, 561
put::Mu *d*(Ap, *lac*) operon fusions, 561
uvrD regulation by the *lexA* product, 1502
secB
E. coli, 253
protein localization, 253
D-Serine deaminase control region
DNA sequence, 1508
E. coli, 1508
Serine protease, cytoplasmic
E. coli, 231
protease So, 231
Sex factor F expression
dye (*sfrA*), 1309
E. coli, 1309
Sialic acid capsular polysaccharide synthesis
N. meningitidis serogroup B, 728
Siderophore activity
Legionella spp. grown in iron-deficient media, 324
Site-directed mutagenesis
plasmid R772::Ti from *A. tumefaciens* in *E. coli*, 693
Slime, extracellular
P. mirabilis swarming, 930
spo0A and *spo0C*
cloned onto phage ρ11, 988
Sporulation
erythromycin, 118
protein synthesis, 118
S. cerevisiae, 118
Staphylococci
transduction efficiency of Tn*551* mediated by methicillin resistance marker, 533
Staphylococcus aureus
computer-assisted chromosome mapping, 395
methicillin resistance
insertional inactivation by Tn*551*, 479
protoplast fusion, 395
protoplast fusion-derived linkages, 406
transformation, 406
ST:LT:CFA/II plasmids
E. coli serogroups O6, O8, O80, O85, O139, 980
Streptococcal R plasmid pIP501, 1347
Streptococci
plasmid curing with protoplasts, 1
Streptococcus faecium
β-lactam inhibition of growth, 916
wall assembly, 573
Streptococcus lactis
2-deoxy-D-glucose, 819
glycolysis, 819
phosphotransferase activities, 819
Streptococcus mutans
oxygen metabolism, 1236
Streptococcus protoplasts
peptidoglycan synthesis, 211
polysaccharide antigen synthesis, 211
Streptococcus pyogenes
hexadecane droplets, adherence to, 139
Streptococcus sanguis
macrolide, lincosamide, streptogramin B resistance, 1252
Streptomyces venezuelae
chloramphenicol production, 239
Sugar phosphotransferase
S. lactis, 819
sulB
allele of *ftsZ*, 1339

E. coli, 1339
Superoxide anion production
C. burnetii, 520
Superoxide dismutase activity
C. burnetii, 520
Swarming
extracellular slime, 930
P. mirabilis, 930
Synechocystis sp. strain PCC 6714
peptidoglycan, 471

Tactic behavior
M. xanthus, 452
Teliospore
partition layer in wall, 499
surface rodlet, 502
T. caries, 499, 502
Thermus sp. strain X-1, 1451
base excision repair, 1451
Tilletia caries
teliospore
partition layer in wall, 499
surface rodlet, 502
Tip structure
M. pneumoniae, 924
TOL pathway regulatory genes, 676
toxA1
P. aeruginosa, 383
Toxigenesis, regulation of
C. diphtheriae mutants, 245
Transduction efficiency
methicillin resistance marker, 533
transposon Tn*551*, 533
Transformability
correlation with deficiency in error-prone repair, 995
Transformation
DNA replication, inhibition of, 686
H. influenzae mutant carrying altered Rec-1 protein, 686
K. lactis killer plasmid DNA, 737
S. aureus, 406
Transposon Tn*551*
methicillin resistance, inactivation, 479
S. aureus, 479
Trichoderma harzianum
lectins, 1431
Trichophyton mentagrophytes
arthrospores
nonfibrillar chitin, 965
Trimethoprim
DNA polymerase deficiency, 1098
E. coli, 1098
trp-his region
B. megaterium, 1455
tsl division initiation gene product
B. subtilis, 537

UDP *N*-acetylglucosamine-enolpyruvate pool levels
correlation with peptidoglycan synthesis, 1284
E. coli, 1284
UDP *N*-acetylglucosamine pool levels
E. coli, 1284
peptidoglycan synthesis, 1284
Unsaturated fatty acid synthesis
E. coli, 554
fadR, 554
UV irradiation
E. coli
mmrA1, 743
uvrD
regulation by the *lexA* product, 1502
S. typhimurium, 1502

Wall assembly
S. faecium, 573

Xylene/toluene catabolism
P. paucimobilis, 1356

Yeast cloning vector
ars from *C. utilis*, 1033
Yeast killer toxin
(1→6)-β-D-glucan, 161
receptor, 161

Zymomonas mobilis
lipid
ethanol, 1291
glucose, 1291